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L2       867434 SEA FILE=REGISTRY SQL<=110
L3           22 SEA FILE=REGISTRY L1 AND L2
L4            8 SEA FILE=HCAPLUS L3


=> d bib abs l4 1-8


L4   ANSWER 1 OF 8  HCAPLUS  COPYRIGHT 2000 ACS
AN   1999:396638  HCAPLUS
DN   131:212774
TI   Mapping of the interleukin-10/interleukin-10 receptor combining site using
     structurally different peptide scans
AU   Reineke, Ulrich; Sabat, Robert; Volk, Hans-Dieter; Schneider-Mergener,
     Jens
CS   Institut fur Medizinische Immunologie, Universitatsklinikum Charite,
     Humboldt-Universitat zu Berlin, Berlin, 10098, Germany
SO   Pept. Proc. Am. Pept. Symp., 15th (1999), Meeting Date 1997, 533-534.
     Editor(s): Tam, James P.; Kaumaya, Pravin T. P. Publisher: Kluwer,
     Dordrecht, Neth.
     CODEN: 67UCAR
DT   Conference
LA   English
AB   The authors describe strategies for the mapping of putative
     interleukin-10/interleukin-10 receptor combining site: (1)the detection of
     low affinity protein-peptide interactions and (2) the use of overlapping
     peptide scans with peptides of different length.

L4   ANSWER 2 OF 8  HCAPLUS  COPYRIGHT 2000 ACS
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AN 1998:250487 HCAPLUS
DN 129:26823
TI Mapping of the interleukin-10/interleukin-10 receptor combining site
AU Reineke, Ulrich; Sabat, Robert; Volk, Hans-Dieter; Schneider-Mergener, Jens
CS Institut fur Medizinische Immunologie, Universitatsklinikum Charite, Humboldt-Universitat zu Berlin, Berlin, 10098, Germany
SO Protein Sci. (1998), 7(4), 951-960
CODEN: PRCIEI; ISSN: 0961-8368
PB Cambridge University Press
DT Journal
LA English
AB The discontinuous interleukin-10 (IL-10)/interleukin-10 receptor (IL-10R) combining site was mapped using sets of overlapping peptides derived from both binding partners bound to continuous cellulose membranes. Low affinity binding of single regions of the discontinuous contact sites on IL-10 and IL-10R could be identified due to (1) high peptide d. on the membrane support, (2) incubation with high protein concns., (3) indirect immunodetection of the ligates after electrotransfer onto polyvinylene difluoride membranes, and (4) use of highly overlapping peptide scans of different length (6-mers and 15-mers). The single binding regions identified for each protein species are sepd. in the protein sequences, but form continuous areas on the surface of IL-10 (x-ray structure) and IL-10R (computer model). Furthermore, 4 epitopes of neutralizing anti-IL-10 and anti-IL-10R antibodies were mapped and overlap with these binding regions. Sol. peptides (15-19-mers) each spanning one of the 3 identified IL-10-derived receptor binding regions displayed no affinity to IL-10R as expected, whereas a peptide (35-mer) comprising two of these regions had considerably higher binding activity. The data are consistent with a previously published computer model of the IL-10/IL-10R complex. This approach should be generally applicable for the mapping of non-linear protein-protein contact sites.

L4 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1998:151218 HCAPLUS
DN 128:150400
TI Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
IN Bult, Carol J.; White, Owen R.; Smith, Hamilton O.; Woese, Carl R.; Venter, J. Craig
PA Institute for Genomic Research, USA; Board of Trustees of the University of Illinois; Johns Hopkins University School of Medicine
SO PCT Int. Appl., 615 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9807830	A2	19980226	WO 1997-US14900	19970822

W: CA, JP
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1996-24428 19960822
AB The present application describes the complete 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements. Also described are 1738

predicted protein-coding genes. Computer-readable media for the storage, search and retrieval of the M. jannaschii genome sequence are also provided.

L4 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1998:26596 HCAPLUS
DN 128:126882
TI Identification of functional domains on human interleukin 10
AU Gesser, Borbala; Leffers, Henrik; Jinquan, Tan; Vestergaard, Christian; Kirstein, Nicka; Sindet-Pedersen, Steen; Lindkaer Jensen, Steen; Thestrup-Pedersen, Kristian; Gronhoj Larsen, Christian
CS Department Dermatology, Marselisborg Hospital, University Aarhus, Aarhus, DK-8000, Den.
SO Proc. Natl. Acad. Sci. U. S. A. (1997), 94(26), 14620-14625
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Interleukin 10 (IL-10) is a recently described natural endogenous immunosuppressive cytokine that has been identified in humans, mice, and other organisms. Human IL-10 (hIL-10) has high homol. with murine IL-10 (mIL-10) as well as with an Epstein-Barr virus genome product BCRFI. This viral IL-10 (vIL-10) shares a no. of activities with hIL-10. IL-10 affects chemokine biol., because human IL-10 inhibits chemokine prodn. and is a specific chemotactic factor for CD8+ T cells. It suppresses the ability of CD4+ T cells, but not CD8+ T cells, to migrate in response to IL-8. A nonapeptide (IT9302) with complete homol. to a sequence of hIL-10 located in the C-terminal portion (residues 152-160) of the cytokine was found to possess activities that mimic some of those of hIL-10. These are: (1) inhibition of IL-1.beta.-induced IL-8 prodn. by peripheral blood mononuclear cell, (2) inhibition of spontaneous IL-8 prodn. by cultured human monocytes, (3) induction of IL-1 receptor antagonist protein prodn. by human monocytes, (4) induction of chemotactic migration of CD8+ human T lymphocytes in vitro, (5) desensitization of human CD8+ T cells resulting in an unresponsiveness toward rhIL-10-induced chemotaxis, (6) suppression of the chemotactic response of CD4+ T human lymphocytes toward IL-8, (7) induction of IL-4 prodn. by cultured normal human CD4+ T cells, (8) down-regulation of tumor necrosis factor-.alpha. prodn. by CD8+ T cells, and (9) inhibition of class II major histocompatibility complex antigen expression on IFN-.gamma.-stimulated human monocytes. Another nonapeptide (IT9403) close to the N-terminal part of hIL-10 did not reveal cytokine synthesis inhibitory properties, but proved to be a regulator of mast cell proliferation. Thus, the authors identified 2 functional domains of IL-10 exerting different IL-10 like activities, an observation that suggests that relatively small segments of these signal proteins are responsible for particular biol. functions.

L4 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1997:499202 HCAPLUS
DN 127:160576
TI Synthetic IL-10 analogs
IN Gronhoj Larsen, Christian; Gesser, Borbala
PA Steeno Research Group A/S, Den.; Gronhoj Larsen, Christian; Gesser, Borbala
SO PCT Int. Appl., 101 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9726278	A1	19970724	WO 1996-DK29	19960118
	W: AL, AM, AT, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AZ, BY, KG, KZ, RU, TJ, TM				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9643856	A1	19970811	AU 1996-43856	19960118
	CA 2243275	AA	19970724	CA 1997-2243275	19970116
	WO 9726279	A1	19970724	WO 1997-DK21	19970116
	W: AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	EP 879245	A1	19981125	EP 1997-900549	19970116
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	CN 1226899	A	19990825	CN 1997-193092	19970116
	BR 9707036	A	19990831	BR 1997-7036	19970116
	AU 9713011	A1	19970811	AU 1997-13011	19970118
PRAI	DK 1996-9629	19960118			
	WO 1996-DK29	19960118			
	WO 1997-DK21	19970116			

AB The invention relates to use of a substance or polypeptide according to the formula: X1-X2-X3-Thr-X4-Lys-X5-Arg-X6, wherein X1 is Ala or Gly, X2 is Tyr or Phe, X3, X4 and X5 are independently selected from the group consisting of Met, Ile, Leu and Val; and X6 is selected from the group consisting of Asp, Gln and Glu, optionally at least one of X1, X2, X3, X4, X5 and X6 is independently substituted with non-natural or unusual amino acids and/or the peptide is cyclized and/or the peptide is stabilized and/or the amino terminal amino acid residue is acylated and/or the carboxy terminal amino acid residue is amidated, and peptidomimetics modelled on the basis of the above formula for the prepn. of a pharmaceutical compn. for the redn. of TNF.alpha. prodn. These peptides inhibit IL-8 prodn. by human monocytes and IL-1.beta.-induced IL-8 prodn. in peripheral blood mononuclear cells, chemotactic response of CD4+ T lymphocytes, chemotactic response of human monocytes towards MCAF/MCP-1, class II MHC mol. expression on human monocytes, TNF-.alpha. prodn. in mixed leukocyte, etc. The IL-10 analogs also induce prodn. of IL-1 receptor antagonist protein in human monocytes, chemotaxis of CD8+ T lymphocytes, IL-4 prodn. in CD4+ T lymphocytes, and modulate LPS-induced shock and leukopenia and bile acid-induced pancreatitis. These peptides are useful for treating conditions related to disturbance of a cytokine system, or diseases where macrophages/T-lymphocyte-mediated immune reactions are considered pathogenetically important.

Searched by David Schreiber 308-4292

L4 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1996:516805 HCAPLUS
DN 125:266912
TI Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
AU Bult, Carol J.; White, Owen; Olsen, Gary J.; Zhou, Lixin; Fleischmann, Robert D.; Sutton, Granger G.; Blake, Judith A.; FitzGerald, Lisa M.; Clayton, Rebecca A.; et al.
CS TIGR, Rockville, MD, 20850, USA
SO Science (Washington, D. C.) (1996), 273(5278), 1058-1073
CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB The complete 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements were detd. by whole-genome random sequencing. A total of 1738 predicted protein-coding genes were identified; however, only a minority of these (38%) could be assigned a putative cellular role with high confidence. Although the majority of genes related to energy prodn., cell division, and metab. in M. jannaschii are most similar to those found in bacteria, most of the genes involved in transcription, translation, and replication in M. jannaschii are more similar to those found in eukaryotes.

L4 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1996:133072 HCAPLUS
DN 124:173458
TI Interleukin 10 agonist polypeptides as immunomodulators
IN Groenhoej Larsen, Christian; Gesser, Borbala
PA Nycomed Dak A/s, Den.
SO PCT Int. Appl., 98 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9601318	A1	19960118	WO 1995-DK227	19950607
	W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, CZ, DE, DK, EE, ES, FI, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK				
	RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2194444	AA	19960118	CA 1995-2194444	19950607
	AU 9526121	A1	19960125	AU 1995-26121	19950607
	EP 769054	A1	19970423	EP 1995-920796	19950607
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	CN 1159830	A	19970917	CN 1995-194787	19950607
	BR 9508243	A	19971021	BR 1995-8243	19950607
	HU 76673	A2	19971028	HU 1996-3615	19950607
	JP 10502249	T2	19980303	JP 1995-503628	19950607
	FI 9700009	A	19970304	FI 1997-9	19970102
	NO 9700020	A	19970305	NO 1997-20	19970103

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PRAI DK 1994-800 19940705
WO 1995-DK227 19950607
OS MARPAT 124:173458
AB This invention relates to a polypeptide other than human interleukin 10 which has at least one of the following properties: a) induces inhibition of spontaneous IL-8 prodn. by human monocytes, b) induces inhibition of IL-1.beta. induced IL-8 prodn. by human peripheral blood mononuclear cells (PBMC), c) induces prodn. of interleukin-1 receptor antagonistic protein (IRAP) by human monocytes, d) induces chemotactic migration of CD8+ human T lymphocytes in vitro, e) desensitizes human CD8+ T cells resulting in an unresponsiveness towards rhIL-10, f) suppresses the chemotactic response of CD4+ T human lymphocytes towards IL-8, g) suppresses the chemotactic response of human monocytes towards MCAF/MCP-1, h) does not inhibit class II MHC mol. expression on human monocytes, in contrast to human IL-10, i) induces the prodn. of IL-4 by cultured normal human CD4+ T cells, j) rescued the TNF.alpha. prodn. in human mixed leukocyte reaction. In particular, the invention relates to the nonapeptide Ala-Tyr-Met-Thr-Met-Lys-Ile-Arg-Asn and analogs and variants thereof. In example, the functions of synthetic polypeptide IT9302 were characterized, and antibody against the synthetic polypeptide IT9302 was prepd.

L4 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2000 ACS
AN 1994:453312 HCAPLUS
DN 121:53312
TI Secondary structures of lipid-associating peptides: a Fourier transform infrared study
AU Zhong, Qi; Clark-Lewis, Ian; Cushley, Robert J.
CS Simon Fraser Univ., Burnaby, BC, Can.
SO Pept. Res. (1994), 7(2), 99-106
CODEN: PEREEO; ISSN: 1040-5704
DT Journal
LA English
AB Four peptides from 20 to 28 residues in length were studied by Fourier transform IR (FTIR) spectroscopy in soln. and in complexes with dimyristoylphosphatidylcholine (DMPC). The four peptides included the 20-residue lipid-assocg. peptide, LAP-20, which was predicted to form an amphipathic helical structure in the presence of lipids, and three other peptides whose sequences had less amphipathic helix-forming properties. The complexes were shown by electron microscopy to be discoidal in shape with mean diams. of 21-27 nm. At the concns. used for IR, the peptides appeared to form oligomers consisting of intermol. .beta.-sheets. In the presence of lipids, the amt. of .beta.-structure decreased; however, amts. of .beta.-structure were still approx. equal to amts. of .alpha.-helix. The IR results for LAP-20 contradicted previous CD results that predicted 50%-90% .alpha.-helix in DMPC complexes. Convex constraint anal. (CCA) deconvolution of the CD (CD) spectrum to est. secondary structures predicted amts. of helix similar to those predicted by IR, but there was still substantial disagreement between IR and CD ests. of other secondary structures. For LAP-20 in complexes, CD predicted random structure. Possible physiol. consequences of partial disordering of peptide structures are discussed.

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